

Figure S1. Relationship between predictor variables, across all stimuli. Related to Figure 1 and Table S1. Each data point reflects one phoneme. Corresponding correlation values are also listed in Table S1.

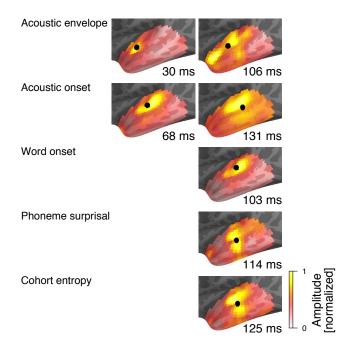


Figure S2. TRF peak maps. Related to Figures 2 and 4 and Table S3. Average of subject maps for all major TRF peaks, averaged in 60 ms windows around peaks. Black circles indicate the center of mass of each map, calculated as described in the Methods section and displayed on Figure 4. See Table S3 for pairwise tests of peak locations.

	ACOUSTIC	ACOUSTIC	Сонокт	Соновт	PHONEME		
	ENVELOPE	ONSET	SIZE	REDUCTION	SURPRISAL		
ACOUSTIC ONSET	.44						
Word-medial							
COHORT SIZE	.0112	.0319					
COHORT REDUCTION	.0112	.0320	.80				
PHONEME SURPRISAL	.0108	.0213	.19	.48			
COHORT ENTROPY	.0011	.0119	.75	.57	.32		
Word-initial							
COHORT SIZE	0700	0305					
COHORT REDUCTION	0700	0304	81				
PHONEME SURPRISAL	0700	0304	.02	.07			
COHORT ENTROPY	0701	0303	.73	78	.19		

Table S1. Predictor correlation. Related to Figure 1. Pairwise correlation for predictor variables across all stimuli. For correlations between the two acoustic predictors, the correlation reflects all samples across time and center frequency. For correlations between acoustic and phoneme-based predictors, correlations were computed separately for each frequency band across all time samples, and the range (min – max) of correlations with the different frequency bands is given. For correlations between phoneme-based variables, correlations between phoneme values, i.e., the values of the non-zero impulses, were computed. Corresponding scatter-plots for phoneme-based variables are displayed in Figure S1.

		Word-medial				Word-initial				
		Cohort	Cohort	Phoneme	Cohort	Cohort	Cohort	Phoneme	Cohort	
		size	reduction	surprisal	entropy	size	reduction	surprisal	entropy	
1	t_{max}	1.47	2.68	3.87**	4.61***	2.21	2.81	2.88	2.54	
	p	.998	.870	.006	< .001	.970	.307	.558	.832	
2	t_{max}		2.95	3.71**	5.10***	2.03	3.37	2.51	2.85	
	p		.517	.006	< .001	.996	.119	.903	.748	
3	t_{max}		3.24	3.95**	4.85***		2.76	2.41	2.50	
	p		.263	.004	< .001		.489	.938	.867	
4	tmax		3.70	3.94**	5.09***		2.78		2.37	
	p		.099	.002	< .001		.417		.967	
5	t_{max}		3.57	3.74**	5.49***		3.40			
	p		.105	.004	< .001		.086			
6	t_{max}			3.98**	6.04***		3.00			
	p			.002	< .001		.397			
7	t_{max}			4.47***	5.68***					
	p			< .001	< .001					

Table S2. Model reduction. Related to Figure 2. Each row constitutes one step in the model reduction. The row provides t_{max} and p-values for each predictor variable (significance marked * \leq .05; ** \leq .01; *** \leq .001). The variable with the lowest non-significant effect size (greatest p-value) was excluded for the next row, until only significant predictor variables remained.

		ACOUSTIC ENVELOPE		ACOUSTIC ONSET		Word	PHONEME
						ONSET	SURPRISAL
		30 ms	106 ms	68 ms	131 ms	103 ms	114 ms
ACOUSTIC ENVELOPE	30 ms						
	106 ms	2					
ACOUSTIC ONSET	68 ms	8**	6				
	131 ms	11***	9***	7**			
WORD ONSET	103 ms	10***	9**	3	5		
PHONEME SURPRISAL	114 ms	5	4	7	7	8*	
COHORT ENTROPY	125 ms	8**	6	7**	4	7**	3

Table S3. Pairwise tests of peak locations. Related to Figures 2 and 4. For each subject, the center of mass of the TRF at a given peak was extracted, and the resulting center coordinates were compared with pairwise permutation-based tests (see Methods section). Each cell displays the distance in mm and corresponding significance test (* \leq .05; *** \leq .01; **** \leq .001). See Figure S2 for average peak distribution maps. Note that center of mass estimates are biased towards the center of the source space volume, and distances are thus smaller than distances between the peaks of average maps.